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A generic model of interactions between FSPM, foliar pathogens and microclimate

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Highlights: A framework was defined to model the interactions between FSPM, foliar fungal pathogens and microclimate, with the concern of interoperability of the components and extensibility. The framework was applied on two existing models of pathosystems (powdery mildew on grapevine and septoria on wheat) to make them more modular and extensible. It will facilitate the design of new disease models on FSPMs.

Keywords: generic modeling, crop architecture, foliar pathogens, powdery mildew, septoria

INTRODUCTION

Functional-structural plant models (FSPMs) are used for the development of increasingly complex simulation models (Cieslak et al. 2011). This reinforces the need to share and reuse submodels in the form of software components (Pradal et al. 2008) and entails standardizing the protocols of communication between them (Fournier et al. 2010). These issues are particularly encountered in epidemiology. The complexity arising from coupling FSPMs with models of fungal foliar pathogens motivated the development of more generic approaches (Mammeri et al. 2010).

Our goal is to design a modular and extensible plant-pathogen model. Two models available on the OpenAlea platform were reviewed: wheat septoria (Robert et al. 2008) and grapevine powdery mildew (Calonnec et al. 2008). The following questions were addressed: What information must the FSPM and pathogen models exchange? Can we identify processes that are common to most foliar pathogens? What levels of detail of plant representation are relevant to model diseases? How to manage different spatial and temporal scales between plant and pathogen?

Beyond demonstrating a practical application of our model, focusing on these contrasted pathosystems aims to prove its adaptability.

DESIGN OF THE MODEL

A pathosystem comprises three main entities: the functional-structural crop, the pathogen population and the physical environment. Each model operating on these entities has its own temporal and spatial scales, while models share a number of variables. For the sake of modularity, we first ensured that each component of the system could be modified independently, without altering the functioning of the others. To do so, we based our model on the generic principles proposed in OpenAlea for exchanging information between components (Fournier et al. 2010). A central data structure representing the canopy at different scales: the Multiscale Tree Graph (MTG: Godin and Caraglio, 1998) is used to circulate variables computed between models (Fig. 1 – See legend). This makes it possible to simulate plant-pathogen interactions such as the competition for a common resource.

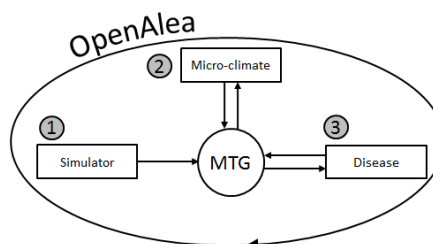


Fig. 1. Schematic of the protocol of communication between pathogen – FSPM – climate through a central data structure representing the canopy (i.e. MTG). At each time step, plant related models update properties of the MTG. Physical models, compute the micro-environment and store it as new MTG properties. These variables are read in the MTG by the fungal model which, in turn, writes new information to the MTG. This information is then used by the plant or physical models to complete their computation.

Consistency of spatial scales

The multi-scale structure of the MTGs is used to access plant and environmental variables at both very fine and coarse scales. The discretization of the plant in our model (phyto-element) is flexible depending on the processes that are modeled and the significance of differences in local values. It is relevant to identify zones on the plant that are homogeneous for variables of interest, and associate the pathogen model at this scale in the MTG. For powdery mildew, a phyto-element was a whole vine leaf; for septoria, a phyto-element was a short (2 cm) sector of wheat leaf.

Definition of generic protocols for disease models interacting with the FSPM

The model for the fungal system can be broken down into the following generic submodels (Fig. 2): initiation of the disease, lesion growth and update, coordination of surface distribution in case of competition, dispersal of spores, and management of nutrients in the phyto-element as a function of fungal uptake. Even if considerable variation exists in the modeling of such processes, it is believed that most foliar pathogens can be modeled by a combination of these submodels. Standardized protocols have been designed for each of them and will not change when passing from one fungus to another or from a complex to a simpler model.

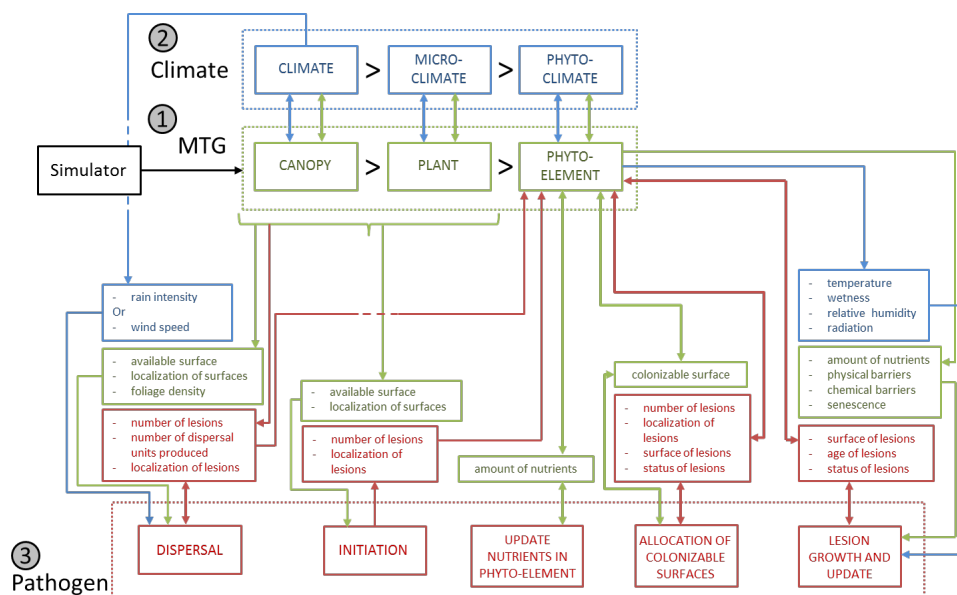


Fig. 2. Relationships between the MTG (green), the pathogen (red) and climate (blue) in the model

Definition of template classes for the disease

Foliar pathogens share common structural features for which a common scheme can be proposed. Diseases are spread by dispersal units and generic symptoms are lesions on leaves. In the model, all lesions on a given phyto-element share the same environmental variables, yet each lesion is treated individually. ‘DispersalUnit’ and ‘Lesion’ have been defined as virtual classes whose interfaces include methods and properties shared by all foliar pathogens. This still leaves great latitude to specialize methods representing a specific disease within the class.

Management of temporal scales

In our study cases, the progress of an individual lesion in physiological age (i.e. cumulation of favorable conditions) and surface is modeled by a continuous growth curve. This curve is modulated by external conditions. Three different temporal scales thus intermingle in our model: the continuous time of plant growth, the continuous time of lesion development and the discrete time of dispersal events. OpenAlea provides tools to coordinate and schedule the different components. Computations for updating plants and lesions are performed on a regular basis, and the intervals are interrupted if necessary when a discrete dispersal event occurs.

IMPLEMENTATION OF TWO PATHOSYSTEM MODELS

The models of Robert et al. (2008) for wheat septoria and Calonnec et al. (2008) for grapevine powdery mildew were re-implemented within the framework described above. Besides demonstrating the applicability

of our approach, this work initiated the development of a library in which formalisms can be picked up for the construction of future models.

In the case of wheat, plant is simulated using Adel-wheat (Fournier et al. 2003) whereas grapevine is simulated by an Lsystem based on TopVine (Louarn et al. 2008). L-Py is used for the generic generation of a MTG from an Lsystem string. Microclimate is simulated using Caribu and RATP.

Adel-Septo and the powdery mildew models were broken down into reusable components:

- The protocol of initiation consists of instantiating primary lesions on leaves (artificial or natural inoculation).
- Each lesion inherits from the class '*Lesion*' with its interface. The surface, the development stage and the rate of production of new dispersal units evolve with the physiological age of the lesion according to pathogen-dependent rules. Each fungus is described by a set of parameters, and specific methods were designed into the classes '*Septoria(Lesion)*' and '*PowderyMildew(Lesion)*' to account for different development mechanisms.
- For both diseases, an additional module coordinates the growth of lesions as a function of healthy surface on leaves that can still be colonized.
- Dispersal is very different between the two chosen pathogens but always occurs in 3 phases: liberation of dispersal units, transport and deposit. Septoria dispersal is a vertical phenomenon triggered by rain splash. The 1D dispersal model from AdelSepto was retrieved and wrapped to comply with the new generic protocol. Dispersal units are rain droplets containing spores. In contrast, powdery mildew dispersal is horizontal according to wind direction. A PlantGL algorithm computes the intersection of a cone with the scene and estimates individual spore deposits. In both cases, each deposited '*DispersalUnit*' will potentially give rise to a new instantiation of a '*Lesion*'.

The outputs of the new wheat model were compared to those of Septo3D giving consistent results. The interoperability of the system components was demonstrated by the instantiation and development of powdery lesions on wheat.

DISCUSSION

With our methodology, two existing models of foliar pathogens have been made more modular and extensible. Reusable disease components were identified and they can be modified without having to change the plant model. We expect the design of new disease models to be accelerated within our framework. The integration of other pathosystems will be necessary to confirm the choices made or to detect limits in the genericity of our approach.

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